



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 03:34 am BST

PDB ID : 6UE0  
Title : Crystal structure of dihydrodipicolinate synthase from *Klebsiella pneumoniae* bound to pyruvate  
Authors : Impey, R.E.; Lee, M.; Hawkins, D.A.; Sutton, J.M.; Panjikar, S.; Perugini, M.A.; Soares da Costa, T.P.  
Deposited on : 2019-09-20  
Resolution : 1.89 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

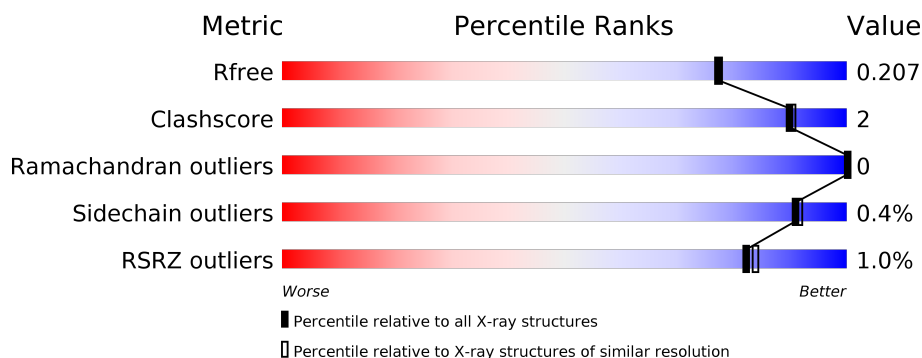
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AAA	326	
1	BBB	326	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4821 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 4-hydroxy-tetrahydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	292	Total	C	N	O	S	0	1	0
			2188	1372	380	420	16			
1	BBB	292	Total	C	N	O	S	0	3	0
			2194	1376	380	422	16			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-33	MET	-	expression tag	UNP W9BBZ5
AAA	-32	GLY	-	expression tag	UNP W9BBZ5
AAA	-31	SER	-	expression tag	UNP W9BBZ5
AAA	-30	SER	-	expression tag	UNP W9BBZ5
AAA	-29	HIS	-	expression tag	UNP W9BBZ5
AAA	-28	HIS	-	expression tag	UNP W9BBZ5
AAA	-27	HIS	-	expression tag	UNP W9BBZ5
AAA	-26	HIS	-	expression tag	UNP W9BBZ5
AAA	-25	HIS	-	expression tag	UNP W9BBZ5
AAA	-24	HIS	-	expression tag	UNP W9BBZ5
AAA	-23	SER	-	expression tag	UNP W9BBZ5
AAA	-22	SER	-	expression tag	UNP W9BBZ5
AAA	-21	GLY	-	expression tag	UNP W9BBZ5
AAA	-20	LEU	-	expression tag	UNP W9BBZ5
AAA	-19	VAL	-	expression tag	UNP W9BBZ5
AAA	-18	PRO	-	expression tag	UNP W9BBZ5
AAA	-17	ARG	-	expression tag	UNP W9BBZ5
AAA	-16	GLY	-	expression tag	UNP W9BBZ5
AAA	-15	SER	-	expression tag	UNP W9BBZ5
AAA	-14	HIS	-	expression tag	UNP W9BBZ5
AAA	-13	MET	-	expression tag	UNP W9BBZ5
AAA	-12	ALA	-	expression tag	UNP W9BBZ5
AAA	-11	SER	-	expression tag	UNP W9BBZ5
AAA	-10	MET	-	expression tag	UNP W9BBZ5
AAA	-9	THR	-	expression tag	UNP W9BBZ5

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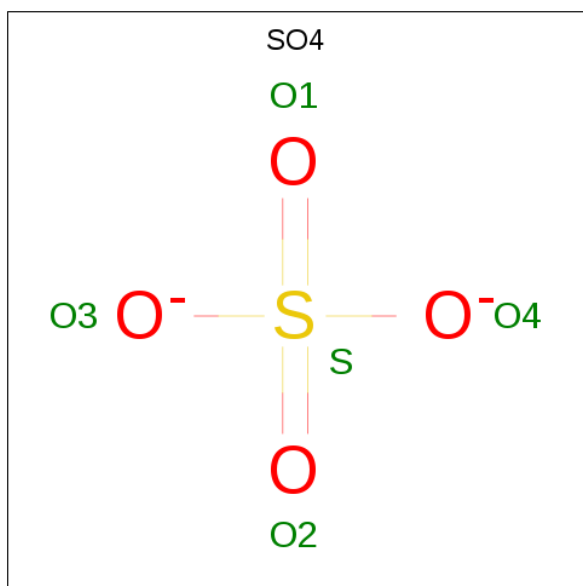
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-8	GLY	-	expression tag	UNP W9BBZ5
AAA	-7	GLY	-	expression tag	UNP W9BBZ5
AAA	-6	GLN	-	expression tag	UNP W9BBZ5
AAA	-5	GLN	-	expression tag	UNP W9BBZ5
AAA	-4	MET	-	expression tag	UNP W9BBZ5
AAA	-3	GLY	-	expression tag	UNP W9BBZ5
AAA	-2	ARG	-	expression tag	UNP W9BBZ5
AAA	-1	GLY	-	expression tag	UNP W9BBZ5
AAA	0	SER	-	expression tag	UNP W9BBZ5
BBB	-33	MET	-	expression tag	UNP W9BBZ5
BBB	-32	GLY	-	expression tag	UNP W9BBZ5
BBB	-31	SER	-	expression tag	UNP W9BBZ5
BBB	-30	SER	-	expression tag	UNP W9BBZ5
BBB	-29	HIS	-	expression tag	UNP W9BBZ5
BBB	-28	HIS	-	expression tag	UNP W9BBZ5
BBB	-27	HIS	-	expression tag	UNP W9BBZ5
BBB	-26	HIS	-	expression tag	UNP W9BBZ5
BBB	-25	HIS	-	expression tag	UNP W9BBZ5
BBB	-24	HIS	-	expression tag	UNP W9BBZ5
BBB	-23	SER	-	expression tag	UNP W9BBZ5
BBB	-22	SER	-	expression tag	UNP W9BBZ5
BBB	-21	GLY	-	expression tag	UNP W9BBZ5
BBB	-20	LEU	-	expression tag	UNP W9BBZ5
BBB	-19	VAL	-	expression tag	UNP W9BBZ5
BBB	-18	PRO	-	expression tag	UNP W9BBZ5
BBB	-17	ARG	-	expression tag	UNP W9BBZ5
BBB	-16	GLY	-	expression tag	UNP W9BBZ5
BBB	-15	SER	-	expression tag	UNP W9BBZ5
BBB	-14	HIS	-	expression tag	UNP W9BBZ5
BBB	-13	MET	-	expression tag	UNP W9BBZ5
BBB	-12	ALA	-	expression tag	UNP W9BBZ5
BBB	-11	SER	-	expression tag	UNP W9BBZ5
BBB	-10	MET	-	expression tag	UNP W9BBZ5
BBB	-9	THR	-	expression tag	UNP W9BBZ5
BBB	-8	GLY	-	expression tag	UNP W9BBZ5
BBB	-7	GLY	-	expression tag	UNP W9BBZ5
BBB	-6	GLN	-	expression tag	UNP W9BBZ5
BBB	-5	GLN	-	expression tag	UNP W9BBZ5
BBB	-4	MET	-	expression tag	UNP W9BBZ5
BBB	-3	GLY	-	expression tag	UNP W9BBZ5
BBB	-2	ARG	-	expression tag	UNP W9BBZ5
BBB	-1	GLY	-	expression tag	UNP W9BBZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
BBB	0	SER	-	expression tag	UNP W9BBZ5

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	O	S	0	0
			5	4	1		
2	BBB	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	BBB	3	Total	Cl	0	0
			3	3		
3	AAA	3	Total	Cl	0	0
			3	3		

- Molecule 4 is water.

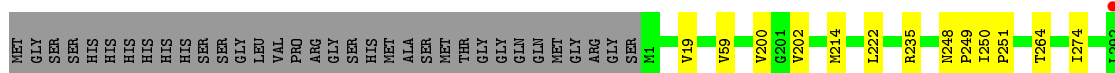
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	218	Total	O	0	0
			218	218		
4	BBB	205	Total	O	0	0
			205	205		

### 3 Residue-property plots


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

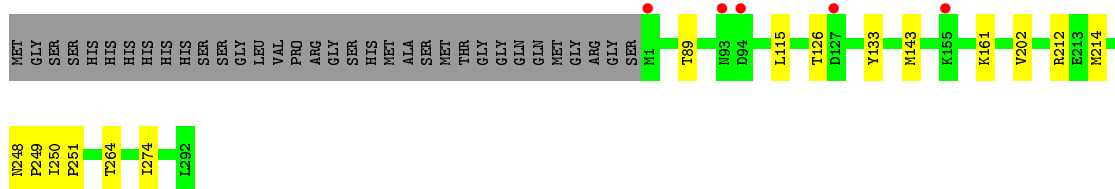
- Molecule 1: 4-hydroxy-tetrahydronicotinate synthase

Chain AAA: 



- Molecule 1: 4-hydroxy-tetrahydronicotinate synthase

Chain BBB: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.63 Å   114.23 Å   55.30 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	48.99 – 1.89 48.99 – 1.89	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.99-1.89) 99.7 (48.99-1.89)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 1.90 Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.169   ,   0.198 0.180   ,   0.207	Depositor DCC
$R_{free}$ test set	2562 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.8	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4821	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KPI, SO4, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	AAA	0.66	0/2211	0.75	0/3002
1	BBB	0.67	0/2223	0.75	0/3018
All	All	0.67	0/4434	0.75	0/6020

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AAA	2188	0	2215	7	0
1	BBB	2194	0	2225	9	0
2	AAA	5	0	0	0	0
2	BBB	5	0	0	0	0
3	AAA	3	0	0	0	0
3	BBB	3	0	0	0	0
4	AAA	218	0	0	1	0
4	BBB	205	0	0	0	0
All	All	4821	0	4440	16	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.



The worst 5 of 16 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:235:ARG:HD2	4:AAA:539:HOH:O	2.00	0.60
1:BBB:115:LEU:HD13	1:BBB:143:MET:HE2	1.86	0.57
1:AAA:251:PRO:HA	1:AAA:274:ILE:HD12	1.93	0.49
1:AAA:19:VAL:HG21	1:AAA:59:VAL:HG22	1.94	0.48
1:BBB:251:PRO:HA	1:BBB:274:ILE:HD12	1.94	0.48

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	290/326 (89%)	286 (99%)	4 (1%)	0	100	100
1	BBB	292/326 (90%)	288 (99%)	4 (1%)	0	100	100
All	All	582/652 (89%)	574 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	236/261 (90%)	235 (100%)	1 (0%)	91	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BBB	238/261 (91%)	237 (100%)	1 (0%)	91	91
All	All	474/522 (91%)	472 (100%)	2 (0%)	91	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	264	THR
1	BBB	264	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	KPI	AAA	161	1	10,13,14	2.51	1 (10%)	6,15,17	2.07	2 (33%)
1	KPI	BBB	161	1	10,13,14	2.82	1 (10%)	6,15,17	1.10	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KPI	AAA	161	1	-	0/9/14/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KPI	BBB	161	1	-	0/9/14/16	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	161	KPI	CX2-CX1	-8.75	1.38	1.52
1	AAA	161	KPI	CX2-CX1	-7.65	1.40	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	161	KPI	C1-CX1-CX2	4.20	122.58	117.92
1	AAA	161	KPI	C1-CX1-NZ	-2.13	117.80	123.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	BBB	161	KPI	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	AAA	301	-	4,4,4	0.30	0	6,6,6	0.09	0
2	SO4	BBB	301	-	4,4,4	0.21	0	6,6,6	0.14	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	AAA	291/326 (89%)	-0.10	1 (0%) 94 94	16, 21, 35, 47	0
1	BBB	291/326 (89%)	-0.06	5 (1%) 70 72	16, 22, 37, 48	0
All	All	582/652 (89%)	-0.08	6 (1%) 82 84	16, 22, 36, 48	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	155	LYS	3.2
1	AAA	292	LEU	2.9
1	BBB	94	ASP	2.6
1	BBB	127	ASP	2.3
1	BBB	93	ASN	2.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
1	KPI	AAA	161	14/15	0.93	0.10	16,17,21,22	0
1	KPI	BBB	161	14/15	0.94	0.11	16,18,25,26	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	BBB	301	5/5	0.96	0.10	27,35,37,38	0
3	CL	AAA	303	1/1	0.98	0.06	26,26,26,26	0
2	SO4	AAA	301	5/5	0.98	0.14	29,41,42,43	0
3	CL	BBB	304	1/1	0.99	0.04	30,30,30,30	0
3	CL	AAA	304	1/1	0.99	0.06	33,33,33,33	0
3	CL	AAA	302	1/1	0.99	0.07	24,24,24,24	0
3	CL	BBB	303	1/1	1.00	0.06	23,23,23,23	0
3	CL	BBB	302	1/1	1.00	0.06	20,20,20,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.